



## RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number: 10/080,114  
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Date Processed by STIC: 3-8-2002

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

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Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Tw , 2011 South Clark Place, Arlington, VA 22202
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Revised 01/29/2002



Does Not Comply  
Corrected Diskette Needed

OIPE

RAW SEQUENCE LISTING      DATE: 03/08/2002  
PATENT APPLICATION: US/10/080,114      TIME: 14:17:01

Input Set : A:\EP.txt  
Output Set: N:\CRF3\03082002\J080114.raw

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4 <110> APPLICANT: Dhugga, Kanwarpal S.
5      Niu, Xiaomu
6      Helentjaris, Timothy
8 <120> TITLE OF INVENTION: Manipulation of Sucrose Synthase Genes
9      to Improve Stalk and Grain Quality
12 <130> FILE REFERENCE: 1301
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/080,114
C--> 14 <141> CURRENT FILING DATE: 2002-02-21
14 <150> PRIOR APPLICATION NUMBER: 60/270,777
15 <151> PRIOR FILING DATE: 2001-02-22
17 <160> NUMBER OF SEQ ID NOS: 13
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0

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## ERRORED SEQUENCES

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21 <210> SEQ ID NO: 1
22 <211> LENGTH: 2737
23 <212> TYPE: DNA
24 <213> ORGANISM: Zea mays
26 <400> SEQUENCE: 1
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W--> 28 60gtctccctc ctgtccaagt acgtgaacaa ggggaaggcg atcctgcage cgcaccacat
W--> 29 120ctctcgacgcg ctgcacgagg tccagggtct cggggggcgc gcctagccg agggaccctt
W--> 30 180ctctcgacgtc ctccgcctcg cgcaggagcg gatcgtgctg cgcgcgttgc ttggccatcg
W--> 31 240aggtgcgcgc cgcgcgggag ttggggagta cgtccgcgtc aacgttcaac agctcagcgt
W--> 32 300cagcagcgtc acagtctcgg agtaccctcg ctccaaggag gagcttgctg accggccagca
W--> 33 360caatgatccc tacgttctcg agcttgactt cgagccgttc aatgtctcag tcccacgccc
W--> 34 420aaatcggtca tcatctattg gaaacggtgt cgagttcttc aaccgacact tgctctcaat
W--> 35 480catgtttccg aacaggggatt gcttgaggcc cctgttggtt ttctccctgt gccaccggca
W--> 36 540caaggggcat gttatgatgc ttaatgatag aatacaaaag ttggggaggc ttcagtctgt
W--> 37 600ctgacccaaa gctgaggagc acttgctcaa gctccctgct gacacaccat actcaaat
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W--> 42 900ggaccaactc cgtgcactag aaaaatgagat ggttctccgt ttaaaagaa aagggttga
W--> 43 960gttttcccca aagatttcca ttgttactcg gctgatacca gatcaaaaag gaacatcatg
W--> 44 1020aatcagcgg cttgagagaa ttagtggaac acagcatact tacatattac gagttccctt
W--> 45 1080gagaatgaa aatgggatac ttaagaatat gatatacaga ttgtatgtgt ggcctatcat
W--> 46 1140gaaacattt cgtgaggatg ctgctgtgtg aattgctgct gaattacaga gtactacaga
W--> 47 1200ttcataatt ggaactaca gtgatggaaa tctgtggcgc tcatgtctat tctacaagat
W--> 48 1260gggaattacc cagtgcacaa ttgctcatgc tctggaaaag actaagtatc cagattcaga

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*number needs to be moved to right hand margin*

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Input Set : A:\EP.txt

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W--> 49 1320 catattttgg aagaatttcg atgagaagta ccatattctcc tgccagtcca ctgctgatat  
W--> 50 1380 aattgctatg aacaatgctg attttatcat caccagcaca taccagaaga ctgctggaag  
W--> 51 1440 aaaaaatact gttggacagt atgagagtea tactgccttt actctgcctg gctctgaccg  
W--> 52 1500 agttgtccat gggatcgatg tcttcgatcc aaagtccaat atagctcttc ctggagctga  
W--> 53 1560 atgtgccata tactttccac ataccgagaa ggccaagcga ccaacctctc ttcatgctga  
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W--> 56 1740 cgtggtcgaa gcttttgcta agtcgcttaa gctgagggag ctgtgaaacc ttgtcgtcgt  
W--> 57 1800 gccgggttac aatgatgta acaagtcгаа ggacagggaa gagatgcggg agatagagaa  
W--> 58 1860 gatgcataa ctcataaaga cccacaactt gttcgggcag ttcgctgga tctctgccca  
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W--> 60 1980 ggtacagcgc gctctgtatg aagcgttcgg tctcaccgtc gttgagcca tgacctgtg  
W--> 61 2040 gcttctactt ttcgcgagcg tccatggagg tccagctgag atcatagagc atggcgtctc  
W--> 62 2100 gggcttccac attgacctgt accaccgca acaggctgtt aatctgatgg ccgacttctt  
W--> 63 2160 gcagcggctgc aagcaagacc cagatcactg ggtgaatata tctggagcac ggtcgagcgg  
W--> 64 2220 catatacag aagtacacat ggaagatata ctcagagagg ttgatgcac tggccggggt  
W--> 65 2280 ctacggtttc tggaaagtac tgcgaagctc cgagagggct gagacagagg gctaccttta  
W--> 66 2340 gatgtctac atactgaagt tccgcgagct ggccaagacc atgtgcctgt caattgacca  
W--> 67 2400 accgcagtag ctgcgcacac tgcgactcgc tagcacttgg tacaagactg aaacctgaag  
W--> 68 2460 gaccttcagt aatttaggcg cggcagagcg tagccaataa aatgtgcggg agctgacctg  
W--> 69 2520 gtttttttat atgtacataa tggcagatata acaaaatac tgaaggcagg tgggttgacg  
W--> 70 2580 tctgtgtgtc gttactgttt actgtattat gtcgaagctt cggctgcgat tctttgtg  
W--> 71 2640 gcaagccgca ggcactgggt aagtgtgat aaatacata tattctgttg acctgtgaaa  
E--> 72 2700 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa cgccgcgc

74 <210> SEQ ID NO: 2  
75 <211> LENGTH: 802  
76 <212> TYPE: PRS  
77 <213> ORGANISM: Zea mays  
79 <400> SEQUENCE: 2

80 Ser Thr His Ala Ser Gly Asp Arg Val Glu Asp Thr Leu His Ala His I  
E--> 81 5 10 15 20 25 Arg Asn Glu Leu Val Ala Leu Leu  
82 Ser Lys Tyr Val Asn Lys Gly Lys 20 25  
E--> 83 30 Gly Ile Leu Gln Pro His His Ile Leu Asp Ala Leu Asp Gly Val Gln  
E--> 84 35 40 45 Gly Ser Gly Gly Arg Ala  
85 Leu Ala Gly Gly Pro Phe Leu Asp Val Leu 50 55  
E--> 86 60 Arg Ser Ala Gln Glu Ala Ile Val Leu Pro Pro Phe Val Ala Ile  
E--> 87 Ala65 70 75 80 Val Arg Pro  
88 Arg Pro Gly Val Trp Glu Tyr Val Arg Val Asn Val His 85  
E--> 89 90 95 Glu Leu Ser Val Glu Gln Leu Thr Val Ser Glu Tyr Leu  
E--> 90 Arg Phe Lys 100 105 110 Glu  
91 Glu Leu Val Asp Gly Gln His Asn Asp Pro Tyr Val Leu Glu Leu 115  
E--> 92 120 125 Asp Phe Glu Pro Phe Asn Val Ser Val Pro Arg  
93 Pro Asn Arg Ser Ser 130 135 140  
94 Ser Ile Gly Asn Gly Val Gln Phe Leu Asn Arg His Leu Ser Ser Ile145  
E--> 95 150 155 160 Met Phe Arg Asn Arg Asp Cys Leu Glu  
96 Pro Leu Leu Asp Phe Leu Arg 165 170  
E--> 97 175 Gly His Arg His Lys Gly His Val Met Met Leu Asn Asp Arg Ile Gln  
E--> 98 180 185 190 Ser Leu Gly Arg Leu Glu Ser  
99 val Leu Thr Lys Ala Glu Glu His Leu 195 200

2737

this is correct location  
for nucleotide numbering

The type of errors shown exist throughout  
the Sequence Listing. Please check subsequent  
sequences for similar errors.

Major format error in  
Amino acid Sequences. USE MAX  
of 16 amino acids per line with  
numbering under every 5th amino acid 3/8/02

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/10/080,114

DATE: 03/08/2002  
 TIME: 14:17:01

Input Set : A:\EP.txt  
 Output Set : N:\CRF3\03082002\J080114.raw

*see page 2*

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E--> 100 205          Ser Lys Leu Pro Ala Asp Thr Pro Tyr Ser Gln Phe Ala Tyr Lys Phe
E--> 101 210          215          220          Gln Gln Trp Gly Leu
      102 Glu Lys Gly Trp Gly Asp Thr Ala Gly His Val225      230
E--> 103 235          240 Leu Glu Met Ile His Leu Leu Leu Asp Ile Ile Gln Ala Pro
E--> 104 Asp Pro      245          250          255          Ser Thr
      105 Leu Glu Lys Phe Leu Gly Arg Ile Pro Met Ile Phe Asn Val      260
E--> 106 265          270          Val Val Val Ser Pro His Gly Tyr Phe Gly Gln Ala
      107 Asn Val Leu Gly      275          280          285
      108 Leu Pro Asp Thr Gly Gly Gln Ile Val Tyr Ile Leu Asp Gln Val Arg      290
E--> 109 295          300          Ala Leu Glu Asn Glu Met Val Leu Arg Leu
      110 Lys Lys Gln Gly Leu Asp305      310          315
E--> 111 320 Val Ser Pro Lys Ile Leu Ile Val Thr Arg Leu Ile Pro Asp Ala Lys
E--> 112 325          330          335          Gly Thr Ser Cys Asn Gln Arg Leu
      113 Glu Arg Ile Ser Gly Thr Gln His      340          345
E--> 114 350          Thr Tyr Ile Leu Arg Val Pro Phe Arg Asn Glu Asn Gly Ile Leu Lys
E--> 115 355          360          365          Lys Trp Ile Ser Arg Phe
      116 Asp Val Trp Pro Tyr Leu Glu Thr Phe Ala      370          375
E--> 117 380          Glu Asp Ala Ala Gly Glu Ile Ala Ala Glu Leu Gln Gly Thr Pro
E--> 118 Asp385      390          395          400 Phe Ile Ile
      119 Gly Asn Tyr Ser Asp Gly Asn Leu Val Ala Ser Leu Leu      405
E--> 120 410          415          Ser Tyr Lys Met Gly Ile Thr Gln Cys Asn Ile Ala His
E--> 121 Ala Leu Glu      420          425          430          Lys
      122 Thr Lys Tyr Pro Asp Ser Asp Ile Phe Trp Lys Asn Phe Asp Glu      435
E--> 123 440          445          Lys Tyr His Phe Ser Cys Gln Phe Thr Ala Asp
      124 Ile Ile Ala Met Asn      450          455
      125 Asn Ala Asp Phe Ile Ile Thr Ser Thr Tyr Gln Glu Ile Ala Gly Ser465
E--> 126 470          475          480 Lys Asn Thr Val Gly Gln Tyr Glu Ser
      127 His Thr Ala Phe Thr Leu Pro      485          490
E--> 128 495          Gly Leu Tyr Arg Val Val His Gly Ile Asp Val Phe Asp Pro Lys Phe
E--> 129 500          505          510          Asn Ile Val Ser Pro Gly Ala
      130 Asp Met Ser Ile Tyr Phe Pro His Thr      515          520
E--> 131 525          Glu Lys Ala Lys Arg Leu Thr Ser Leu His Gly Ser Ile Glu Asn Leu
E--> 132 530          535          540          Ile Tyr Asp Pro Glu
      133 Gln Asn Asp Glu His Ile Gly His Leu Asp Asp545      550
E--> 134 555          560 Arg Ser Lys Pro Ile Leu Phe Ser Met Ala Arg Leu Asp Arg
E--> 135 Val Lys      565          570          575          Asn Ile
      136 Thr Gly Leu Val Glu Ala Phe Ala Lys Cys Ala Lys Leu Arg      580
E--> 137 585          590          Glu Leu Val Asn Leu Val Val Val Ala Gly Tyr Asn
      138 Asp Val Asn Lys      595          600          605
      139 Ser Lys Asp Arg Glu Glu Ile Ala Glu Ile Glu Lys Met His Glu Leu      610
E--> 140 615          620          Ile Lys Thr His Asn Leu Phe Gly Gln Phe
      141 Arg Trp Ile Ser Ala Gln625      630          635
E--> 142 640 Thr Asn Arg Ala Arg Asn Gly Glu Leu Tyr Arg Tyr Ile Ala Asp Thr
E--> 143 645          650          655          His Gly Ala Phe Val Gln Pro Ala
      144 Leu Tyr Glu Ala Phe Gly Leu Thr      660          665
E--> 145 670          Val Val Glu Ala Met Thr Cys Gly Leu Pro Thr Phe Ala Thr Leu His
E--> 146 675          680          685          Gly Gly Pro Ala Glu Ile
      147 Ile Glu His Gly Val Ser Gly Phe His Ile      690          695
E--> 148 700          Asp Pro Tyr His Pro Glu Gln Ala Val Asn Leu Met Ala Asp Phe

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E--> 149 Phe705 710 715 720 Asp Arg Cys  
 150 Lys Gln Asp Pro Asp His Trp Val Asn Ile Ser Gly Ala 725  
 E--> 151 730 735 Gly Leu Gln Arg Ile Tyr Glu Lys Tyr Thr Trp Lys Ile  
 E--> 152 Tyr Ser Glu 740 745 750 Arg  
 153 Leu Met Thr Leu Ala Gly Val Tyr Gly Phe Trp Lys Tyr Val Ser 755  
 E--> 154 760 765 Lys Leu Glu Arg Leu Glu Thr Arg Arg Tyr Leu  
 155 Glu Met Phe Tyr Ile 770 775 780  
 156 Leu Lys Phe Arg Glu Leu Ala Lys Thr Val Pro Leu Ala Ile Asp Gln785  
 E--> 157 790 795 800 Pro Gln  
 392 <210> SEQ ID NO: 5  
 393 <211> LENGTH: 802  
 394 <212> TYPE: PRT  
 395 <213> ORGANISM: Zea mays  
 397 <400> SEQUENCE: 5  
 398 Met Ala Ala Lys Leu Thr Arg Leu His Ser Leu Arg Glu Arg Leu Gly 1  
 E--> 399 5 10 15 Ala Thr Phe Ser Ser His Pro Asn  
 400 Glu Leu Ile Ala Leu Phe Ser Arg 20 25  
 E--> 401 30 Tyr Val His Gln Gly Lys Gly Met Leu Gln Arg His Gln Leu Leu Ala  
 E--> 402 35 40 45 Glu Phe Asp Ala Leu Phe  
 403 Asp Ser Asp Lys Glu Lys Tyr Ala Pro Phe 50 55  
 E--> 404 60 Glu Asp Ile Leu Arg Ala Ala Gln Glu Ala Ile Val Leu Pro Pro  
 E--> 405 Trp65 70 75 80 val Ala Leu  
 406 Ala Ile Arg Pro Arg Pro Gly Val Trp Asp Tyr Ile Arg 85  
 E--> 407 90 95 Val Asn Val Ser Glu Leu Ala Val Glu Glu Leu Ser Val  
 E--> 408 Ser Glu Tyr 100 105 110 Leu  
 409 Ala Phe Lys Glu Gln Leu Val Asp Gly Gln Ser Asn Ser Asn Phe 115  
 E--> 410 120 125 Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Ala  
 411 Ser Phe Pro Arg Pro 130 135 140  
 412 Ser Met Ser Lys Ser Ile Gly Asn Gly Val Gln Phe Leu Asn Arg His145  
 E--> 413 150 155 160 Leu Ser Ser Lys Leu Phe Gln Asp Lys  
 414 Glu Ser Leu Tyr Pro Leu Leu 165 170  
 E--> 415 175 Asn Phe Leu Lys Ala His Asn Tyr Lys Gly Thr Thr Met Met Leu Asn  
 E--> 416 180 185 190 Asp Arg ile Gln Ser Ser Leu Arg  
 417 Gly Leu Gln Ser Ser Leu Arg Lys Ala 195 200  
 E--> 418 205 Glu Gly Tyr Leu Leu Ser Val Pro Gln Asp Thr Pro Tyr Ser Glu Phe  
 E--> 419 210 215 220 Asn His Arg Phe Gln  
 420 Glu Leu Gly Leu Glu Lys Gly Trp Gly Asp Thr225 230  
 E--> 421 235 240 Ala Lys Arg Val Leu Asp Thr Leu His Leu Leu Leu Asp Leu  
 E--> 422 Leu Glu 245 250 255 Ala Pro  
 423 Asp Pro Ala Asn Leu Glu Lys Phe Leu Gly Thr Ile Pro Met 260  
 E--> 424 265 270 Met Phe Asn Val Val Ile Leu Ser Pro His Gly Tyr  
 425 Phe Ala Gln Ser 275 280 285  
 426 Asn Val Leu Gly Tyr Pro Asp Thr Gly Gly Gln Val Val Tyr Ile Leu 290  
 E--> 427 295 300 310 Asp Gln Val Arg Ala Leu Glu Asn Glu Met  
 428 Leu Leu Arg Ile Lys Gln305 315  
 E--> 429 320 Gln Gly Leu Asp Ile Thr Pro Lys Ile Leu Ile Val Thr Arg Leu Leu  
 E--> 430 325 330 335 Pro Asp Ala Ala Gly Thr Thr Cys  
 431 Gly Gln Arg Leu Glu Lys Val Ile 340 345  
 E--> 432 350 Gly Thr Glu His Thr Asp Ile Ile Arg Val Pro Phe Arg Asn Glu Asn

See page 2

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*see page 2*

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E--> 433 355                               360                               365                               Gly Ile Leu Arg Lys Trp
434 Ile Ser Arg Phe Asp Val Trp Pro Tyr Leu                               370                               375
E--> 435 380                               Glu Thr Tyr Thr Glu Asp Val Ser Ser Glu Ile Met Lys Glu Met
E--> 436 Gln385                             390                               395                               400 Ala Lys Pro
437 Asp Leu Ile Ile Gly Asn Tyr Ser Asp Gly Asn Leu Val                               405
E--> 438 410                               415                               Ala Thr Leu Leu Ala His Lys Leu Gly Val Thr Gln Cys
E--> 439 Thr Ile Ala                               420                               425                               430 His
440 Ala Leu Glu Lys Thr Lys Tyr Pro Asn Ser Asp Ile Tyr Leu Asp                               435
E--> 441 440                               445                               Lys Phe Asp Ser Gln Tyr His Phe Ser Cys Gln
442 Phe Thr Ala Asp Leu                               450                               455                               460
443 Ile Ala Met Asn His Thr Asp Phe Ile Ile Thr Ser Thr Phe Gln Glu465
E--> 444 470                               475                               480 Ile Ala Gly Ser Lys Asp Thr Val Gly
445 Gln Tyr Glu Ser His Ile Ala                               485                               490
E--> 446 495                               Phe Thr Leu Pro Gly Leu Tyr Arg Val Val His Gly Ile Asp Val Phe
E--> 447 500                               505                               510                               Asp Pro Lys Phe Asn Ile Val
448 Ser Pro Gly Ala Asp Met Ser Val Tyr                               515                               520
E--> 449 525                               Tyr Pro Tyr Thr Glu Thr Asp Lys Arg Leu Thr Ala Phe His Pro Glu
E--> 450 530                               535                               540                               Ile Glu Glu Leu Ile
451 Tyr Ser Asp Val Glu Asn Ser Glu His Lys Phe545                               550
E--> 452 555                               560 Val Leu Lys Asp Lys Lys Lys Pro Ile Ile Phe Ser Met Ala
E--> 453 Arg Leu                               565                               570                               575 Asp Arg
454 Val Lys Asn Met Thr Gly Leu Val Glu Met Tyr Gly Lys Asn                               580
E--> 455 585                               590                               Ala Arg Leu Arg Glu Leu Ala Asn Leu Val Ile Val
456 Ala Gly Asp His                               595                               600                               605
457 Gly Lys Glu Ser Lys Asp Arg Glu Glu Gln Ala Glu Phe Lys Lys Met                               610
E--> 458 615                               620                               Tyr Ser Leu Ile Asp Glu Tyr Lys Leu Lys
459 Gly His Ile Arg Trp Ile625                               630                               635
E--> 460 640 Ser Ala Gln Met Asn Arg Val Arg Asn Gly Glu Leu Tyr Arg Tyr Ile
E--> 461 645                               650                               655                               Cys Asp Thr Lys Gly Ala Phe Val
462 Gln Pro Ala Phe Tyr Glu Ala Phe                               660                               665
E--> 463 670                               Gly Leu Thr Val Ile Glu Ser Met Thr Cys Gly Leu Pro Thr Ile Ala
E--> 464 675                               680                               685                               Thr Cys His Gly Gly Pro
465 Ala Glu Ile Ile Val Asp Gly Val Ser Gly                               690                               695
E--> 466 700                               Leu His Ile Asp Pro Tyr His Ser Asp Lys Ala Ala Asp Ile Leu
E--> 467 Val705                               710                               715                               720 Asn Phe Phe
468 Asp Lys Cys Lys Ala Asp Pro Ser Tyr Trp Asp Glu Ile                               725
E--> 469 730                               735                               Ser Gln Gly Gly Leu Gln Arg Ile Tyr Glu Lys Tyr Thr
E--> 470 Trp Lys Leu                               740                               745                               750 Tyr
471 Ser Glu Arg Leu Met Thr Leu Thr Gly Val Tyr Gly Phe Trp Lys                               755
E--> 472 760                               765                               Tyr Val Ser Asn Leu Glu Arg Arg Glu Thr Arg
473 Arg Tyr Ile Glu Met                               770                               775                               780
474 Phe Tyr Ala Leu Lys Tyr Arg Ser Leu Ala Ser Gln Val Pro Leu Ser785
E--> 475 790                               795                               800 Phe Asp

703 <210> SEQ ID NO: 7
704 <211> LENGTH: 816
705 <212> TYPE: PRT
706 <213> ORGANISM: Zea mays
708 <400> SEQUENCE: 7
709 Met Gly Glu Gly Ala Gly Asp Arg Val Leu Ser Arg Leu His Ser Val 1

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E--> 710 5          10          15      Arg Glu Arg Ile Gly Asp Ser Leu
711 Ser Ala His Pro Asn Glu Leu Val          20          25
E--> 712 30      Ala Val Phe Thr Arg Leu Lys Asn Leu Gly Lys Gly Met Leu Gln Pro
E--> 713 35          40          45          His Gln Ile Ile Ala Glu
714 Tyr Asn Asn Ala Ile Pro Glu Ala Glu Arg          50          55
E--> 715 60      Glu Lys Leu Lys Asp Gly Ala Phe Glu Asp Val Leu Arg Ala Ala
E--> 716 Gln65          70          75          80 Glu Ala Ile
717 Val Ile Pro Pro Trp Val Ala Leu Ala Ile Arg Pro Arg          85
E--> 718 90          95      Pro Gly Val Trp Glu Tyr Trp Val Arg Val Asn Val Ser Glu
E--> 719 Leu Ala Val          100          105          110          Glu
720 Glu Leu Arg Val Pro Glu Tyr Leu Gln Phe Lys Glu Gln Leu Val          115
E--> 721 120          125          Glu Glu Gly Pro Asn Asn Asn Phe Val Leu Glu
722 Leu Asp Phe Glu Pro          130          135
723 Phe Asn Ala Ser Phe Pro Arg Pro Ser Leu Ser Lys Ser Ile Gly Asn145
E--> 724 150          155          160 Gly Val Gln Phe Leu Asn Arg His Leu
725 Ser Ser Ser Lys Leu Phe His Asp          165          170
E--> 726 175          Lys Glu Ser Met Tyr Pro Leu Leu Asn Phe Leu Arg Ala His Asn Tyr
E--> 727 180          185          190          Lys Gly Met Thr Met Met Leu
728 Asn Asn Arg Arg Ile Arg Ser Leu Ser Ala          195          200
E--> 729 205          Leu Gln Gly Ala Leu Arg Lys Ala Glu Glu His Leu Ser Thr Leu Gln
E--> 730 210          215          220          Ala Asp Thr Pro Tyr
731 Ser Glu Phe His His Arg Phe Gln Glu Leu Gly225          230
E--> 732 235          240 Leu Glu Lys Gly Trp Gly Asp Cys Ala Lys Arg Ala Gln Glu
E--> 733 Thr Ile          245          250          255          His Leu
734 Leu Leu Asp Leu Leu Glu Ala Pro Asp Pro Ser Thr Leu Glu          260
E--> 735 265          270          Lys Phe Leu Gly Thr Ile Pro Met Val Phe Asn Val
736 Val Ile Leu Ser          275          280          285
737 Pro His Gly Tyr Phe Ala Gln Ala Asn Val Leu Gly Tyr Pro Asp Thr          290
E--> 738 295          300          Gly Gly Gln Val Val Tyr Ile Leu Asp Gln
739 Val Arg Ala Met Glu Asn305          310          315
E--> 740 320 Glu Met Leu Leu Arg Ile Lys Gln Cys Gly Leu Asp Ile Thr Pro Lys
E--> 741 325          330          335          Ile Leu Ile Val Thr Arg Leu Leu
742 Pro Asp Ala Thr Gly Thr Thr Cys          340          345
E--> 743 350          Gly Gln Arg Leu Glu Lys Val Leu Gly Thr Glu His Cys His Ile Leu
E--> 744 355          360          365          Arg Val Pro Phe Arg Thr
745 Glu Asn Gly Ile Val Arg Lys Trp Ile Ser          370          375
E--> 746 380          Arg Phe Glu Val Trp Pro Tyr Leu Glu Thr Tyr Thr Asp Asp Val
E--> 747 Ala385          390          395          400 His Glu Ile
748 Ala Gly Glu Leu Gln Ala Asn Pro Asp Leu Ile Ile Gly          405
E--> 749 410          415          Asn Tyr Ser Asp Gly Asn Leu Val Ala Cys Leu Leu Ala
E--> 750 His Lys Met          420          425          430          Gly
751 Val Thr His Cys Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr          435
E--> 752 440          445          Pro Asn Ser Asp Leu Tyr Trp Lys Lys Phe Glu
753 Asp His Tyr His Phe          450          455          460
754 Ser Cys Gln Phe Thr Thr Asp Leu Ile Ala Met Asn His Ala Asp Phe465
E--> 755 470          475          480 Ile Ile Thr Ser Thr Phe Gln Glu Ile
756 Ala Gly Asn Lys Asp Thr Val          485          490
E--> 757 495          Gly Gln Tyr Glu Ser His Met Ala Phe Thr Met Pro Gly Leu Tyr Arg
E--> 758 500          505          510          Val Val His Gly Ile Asp Val

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/080,114

DATE: 03/08/2002

TIME: 14:17:01

Input Set : A:\EP.txt

Output Set: N:\CRF3\03082002\J080114.raw

See page 2

```

759 Phe Asp Pro Lys Phe Asn Ile Val Ser 515 520
E--> 760 525 Pro Gly Ala Asp Leu Ser Ile Tyr Phe Pro Tyr Thr Glu Ser His Lys
E--> 761 530 535 540 Arg Leu Thr Ser Leu
762 His Pro Glu Ile Glu Glu Leu Leu Tyr Ser Gln 545 550
E--> 763 555 560 Thr Glu Asn Thr Glu His Lys Phe Val Leu Asn Asp Arg Asn
E--> 764 Lys Pro 565 570 575 Ile Ile
765 Phe Ser Met Ala Arg Leu Asp Arg Val Lys Asn Leu Thr Gly 580
E--> 766 585 590 Leu Val Glu Leu Tyr Gly Arg Asn Lys Arg Leu Gln
767 Glu Leu Val Asn 595 600 605
768 Leu Val Val Val Cys Gly Asp His Gly Asn Pro Ser Lys Asp Lys Glu 610
E--> 769 615 620 Glu Gln Ala Glu Phe Lys Lys Met Phe Asp
770 Leu Ile Glu Gln Tyr Asn 625 630 635
E--> 771 640 Leu Asn Gly His Ile Arg Trp Ile Ser Ala Gln Met Asn Arg Val Arg
E--> 772 645 650 655 Asn Gly Glu Leu Tyr Arg Tyr Ile
773 Cys Asp Thr Lys Gly Ala Phe Val 660 665
E--> 774 670 Gln Pro Ala Phe Tyr Glu Ala Phe Gly Leu Thr Val Val Glu Ala Met
E--> 775 675 680 685 Thr Cys Gly Leu Pro Thr
776 Phe Ala Thr Ala Tyr Gly Gly Pro Ala Glu 690 695
E--> 777 700 Ile Ile Val His Gly Val Ser Gly Tyr His Ile Asp Pro Tyr Gln
E--> 778 Gly 705 710 715 720 Asp Lys Ala
779 Ser Ala Leu Leu Val Asp Phe Phe Asp Lys Cys Gln Ala 725
E--> 780 730 735 Glu Pro Ser His Trp Ser Lys Ile Ser Gln Gly Gly Leu
E--> 781 Gln Arg Ile 740 745 750 Glu
782 Glu Lys Tyr Thr Trp Lys Leu Tyr Ser Glu Arg Leu Met Thr Leu 755
E--> 783 760 765 Thr Gly Val Tyr Gly Phe Trp Lys Tyr Val Ser
784 Asn Leu Glu Arg Arg 770 775 780
785 Glu Thr Arg Arg Tyr Leu Glu Met Leu Tyr Ala Leu Lys Tyr Arg Thr 785
E--> 786 790 795 800 Met Ala Ser Thr Val Pro Leu Ala Val
787 Glu Gly Glu Pro Ser Ser Lys 805 810
E--> 788 815

```



## VERIFICATION SUMMARY

DATE: 03/08/2002

PATENT APPLICATION: US/10/080,114

TIME: 14:17:02

Input Set : A:\EP.txt

Output Set: N:\CRF3\03082002\J080114.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No  
 L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:27 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:1  
 L:28 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:29 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:29 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:30 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:30 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:31 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:31 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:32 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:32 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:33 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:33 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:34 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:34 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:35 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:35 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:36 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:36 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:37 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:37 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:38 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:38 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:39 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:39 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:40 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:40 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:41 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:41 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:42 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:42 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:43 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:43 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:44 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:44 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:45 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:45 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:46 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:46 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:47 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:47 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:48 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:48 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:49 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:49 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:50 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:50 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/080,114

DATE: 03/08/2002

TIME: 14:17:02

Input Set : A:\EP.txt

Output Set: N:\CRF3\03082002\J080114.raw

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L:51 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:51 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:52 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:52 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:53 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:53 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:54 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:54 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:55 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:55 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:56 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:56 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:57 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:57 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:58 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:58 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:59 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:59 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:60 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:60 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:61 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:61 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:62 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:62 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:63 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:63 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:64 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:64 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:65 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:65 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:66 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:66 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:67 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:67 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:68 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:68 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:69 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:69 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:70 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:70 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:71 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:71 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:72 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
M:254 Repeated in SeqNo=1
L:72 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
L:72 M:252 E: No. of Seq. differs, <211>LENGTH:Input:2737 Found:97 SEQ:1
L:81 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:83 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:83 M:333 E: Wrong sequence grouping, Amino acids not in groups!

```

## VERIFICATION SUMMARY

DATE: 03/08/2002

PATENT APPLICATION: US/10/080,114

TIME: 14:17:02

Input Set : A:\EP.txt

Output Set: N:\CRF3\03082002\J080114.raw

M:332 Repeated in SeqNo=2

L:84 M:333 E: Wrong sequence grouping, Amino acids not in groups!

L:86 M:333 E: Wrong sequence grouping, Amino acids not in groups!

L:87 M:333 E: Wrong sequence grouping, Amino acids not in groups!

L:87 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1

L:89 M:333 E: Wrong sequence grouping, Amino acids not in groups!

L:118 M:333 E: Wrong sequence grouping, Amino acids not in groups!

L:118 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1

L:149 M:333 E: Wrong sequence grouping, Amino acids not in groups!

L:149 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1

L:157 M:252 E: No. of Seq. differs, <211>LENGTH:Input:802 Found:451 SEQ:2

L:399 M:333 E: Wrong sequence grouping, Amino acids not in groups!

L:401 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5

L:401 M:333 E: Wrong sequence grouping, Amino acids not in groups!

M:332 Repeated in SeqNo=5

L:402 M:333 E: Wrong sequence grouping, Amino acids not in groups!

L:404 M:333 E: Wrong sequence grouping, Amino acids not in groups!

L:405 M:333 E: Wrong sequence grouping, Amino acids not in groups!

L:405 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1

L:407 M:333 E: Wrong sequence grouping, Amino acids not in groups!

L:436 M:333 E: Wrong sequence grouping, Amino acids not in groups!

L:436 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1

L:467 M:333 E: Wrong sequence grouping, Amino acids not in groups!

L:467 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1

L:475 M:252 E: No. of Seq. differs, <211>LENGTH:Input:802 Found:451 SEQ:5

L:710 M:333 E: Wrong sequence grouping, Amino acids not in groups!

L:712 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7

L:712 M:333 E: Wrong sequence grouping, Amino acids not in groups!

M:332 Repeated in SeqNo=7

L:713 M:333 E: Wrong sequence grouping, Amino acids not in groups!

L:715 M:333 E: Wrong sequence grouping, Amino acids not in groups!

L:716 M:333 E: Wrong sequence grouping, Amino acids not in groups!

L:716 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1

L:718 M:333 E: Wrong sequence grouping, Amino acids not in groups!

L:747 M:333 E: Wrong sequence grouping, Amino acids not in groups!

L:747 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1

L:778 M:333 E: Wrong sequence grouping, Amino acids not in groups!

L:778 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1

L:788 M:252 E: No. of Seq. differs, <211>LENGTH:Input:816 Found:458 SEQ:7